RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/580,596 _____
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IFWP

RAW SEQUENCE LISTING   DATE: 06/07/2006
PATENT APPLICATION: US/10/580,596   TIME: 11:02:16

Input Set : **A:\70325USPCT Seq List.ST25.txt**
Output Set: **N:\CRF4\06072006\J580596.raw**

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 3 <110> APPLICANT: SYNGENTA PARTICIPATIONS AG
 4        NEGROTTO, David V.
 5        SHOTKOSKI, Frank A.
 6        YU, Wenjin A.
 8 <120> TITLE OF INVENTION: INSECT RESISTANT COTTON PLANTS AND METHODS OF DETECTING THE
SAME
10 <130> FILE REFERENCE: 70325USPCT
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C--> `12 <140> **CURRENT APPLICATION NUMBER: US/10/580,596**`
C--> `12 <141> **CURRENT FILING DATE: 2006-05-25**`
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   12 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/012662
   13 <151> PRIOR FILING DATE: 2004-11-09
   15 <150> PRIOR APPLICATION NUMBER: US 60/526,112
   16 <151> PRIOR FILING DATE: 2003-12-01
   18 <160> NUMBER OF SEQ ID NOS: 18
   20 <170> SOFTWARE: PatentIn version 3.2
   22 <210> SEQ ID NO: 1
   23 <211> LENGTH: 26
   24 <212> TYPE: DNA
   25 <213> ORGANISM: Artificial Sequence
   27 <220> FEATURE:
   28 <223> OTHER INFORMATION: COT202 nucleotide motif
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   35 <211> LENGTH: 26
   36 <212> TYPE: DNA
   37 <213> ORGANISM: Artificial Sequence
   39 <220> FEATURE:
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   42 <400> SEQUENCE: 2
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   48 <212> TYPE: DNA
   49 <213> ORGANISM: Artificial Sequence
   51 <220> FEATURE:
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   60 <212> TYPE: DNA
   61 <213> ORGANISM: Artificial Sequence
   63 <220> FEATURE:
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84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
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107 aagatcgact tcaccaagaa gatgaagacc ctgcgctacg aggtgaccgc caacttctac   180
109 gacagcagca ccggcgagat cgacctgaac aagaagaagg tggagagcag cgaggccgag   240
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116 <212> TYPE: DNA
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123 gatttggagc caagtctcat aaacgccatt gtggaagaaa gtcttgagtt ggtggtaatg   60
125 taacagagta gtaagaacag agaagagaga gagtgtgaga tacatgaatt gtcgggcaac   120
127 aaaaatcctg aacatcttat tttagcaaag agaaagagtt ccgagtctgt agcagaagag   180
129 tgaggagaaa tttaagctct tggacttgtg aattgttccg cctcttgaat acttcttcaa   240
131 tcctcatata ttcttcttct atgttacctg aaaaccggca tttaatctcg cgggtttatt   300
133 ccggttcaac attttttttg ttttgagtta ttatctgggc ttaataacgc aggcctgaaa   360
135 taaattcaag gcccaactgt tttttttttt aagaagttgc tgttaaaaaa aaaaaaaggg   420
137 aattaacaac aacaacaaaa aaagataaag aaaataataa caattacttt aattgtagac   480
139 taaaaaaaca tagattttat catgaaaaaa agagaaaaga aataaaaact tggatcaaaa   540
141 aaaaacatac agatcttcta attattaact tttcttaaaa attaggtcct ttttcccaac   600
143 aattaggttt agagttttgg aattaaacca aaaagattgt tctaaaaaat actcaaattt   660

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147 ttagagtaga ttagaatctt ttatgccaag tattgataaa ttaaatcaag aagataaact    780
149 atcataatca acatgaaatt aaaagaaaaa tctcatatat agtattagta ttctctatat    840
151 atattatgat tgcttattct taatgggttg ggttaaccaa gacatagtct taatggaaag    900
153 aatctttttt gaactttttc cttattgatt aaattcttct atagaaaaga aagaaattat    960
155 ttgaggaaaa gtatatacaa aaagaaaaat agaaaaatgt cagtgaagca gatgtaatgg   1020
157 atgacctaat ccaaccacca ccataggatg tttctacttg agtcggtctt ttaaaaacgc   1080
159 acggtggaaa atatgacacg tatcatatga ttccttcctt tagtttcgtg ataataatcc   1140
161 tcaactgata tcttcctttt tttgttttgg ctaaagatat tttattctca ttaatagaaa   1200
163 agacggtttt gggctttttgg tttgcgatat aaagaagacc ttcgtgtgga agataataat   1260
165 tcatcctttc gtctttttct gactcttcaa tctctcccaa agcctaaagc gatctctgca   1320
167 aatctctcgc gactctctct ttcaaggtat attttctgat tcttttttgtt tttgattcgt   1380
169 atctgatctc caatttttgt tatgtggatt attgaatctt ttgtataaat tgctttttgac   1440
171 aatattgttc gtttcgtcaa tccagcttct aaattttgtc ctgattacta agatatcgat   1500
173 tcgtagtgtt tacatctgtg taatttcttg cttgattgtg aaattaggat tttcaaggac   1560
175 gatctattca attttttgtgt tttctttgtt cgattctctc tgttttaggt ttcttatgtt   1620
177 tagatccgtt tctctttggt gttgttttga tttctcttac ggcttttgat ttggtatatg   1680
179 ttcgctgatt ggtttctact tgttctattg tttttatttca ggtggatcca ccatgaacaa   1740
181 gaacaacacc aagctgagca cccgcgccct gccgagcttc atcgactact caacggcat    1800
183 ctacggcttc gccaccggca tcaaggacat catgaacatg atcttcaaga ccgacaccgg   1860
185 cggcgacctg accctggacg agatcctgaa gaaccagcag ctgctgaacg acatcagcgg   1920
187 caagctggac ggcgtgaacg gcagcctgaa cgacctgatc gcccagggca acctgaacac   1980
189 cgagctgagc aaggagatcc ttaagatcgc caacgagcag aaccaggtgc tgaacgacgt   2040
191 gaacaacaag ctggacgcca tcaacaccat gctgcgcgtg tacctgccga agatcaccag   2100
193 catgctgagc gacgtgatga agcagaacta cgccctgagc ctgcagatcg agtacctgag   2160
195 caagcagctg caggagatca gcgacaagct ggacatcatc aacgtgaacg tcctgatcaa   2220
197 cagcaccctg accgagatca ccccggccta ccagcgcatc aagtacgtga acgagaagtt   2280
199 cgaagagctg accttcgcca ccgagaccag cagcaaggtg aagaaggacg gcagcccggc   2340
201 cgacatcctg gacgagctga ccgagctgac cgagctggcg aagagcgtga ccaagaacga   2400
203 cgtggacggc ttcgagttct acctgaacac cttccacgac gtgatggtgg gcaacaacct   2460
205 gttcggccgc agcgccctga gaccgccag cgagctgatc accaaggaga acgtgaagac   2520
207 cagcggcagc gaggtgggca acgtgtacaa cttcctgatc gtgctgaccg ccctgcaggc   2580
209 ccaggccttc ctgaccctga ccacctgtcg caagctgctg ggcctggccg acatcgacta   2640
211 caccagcatc atgaacgagc acttgaacaa ggagaaggag gagttccgcg tgaacatcct   2700
213 gccgaccctg agcaacacct tcagcaaccc gaactacgcc aaggtgaagg gcagcgacga   2760
215 ggacgccaag atgatcgtgg aggctaagcc gggccacgcg ttgatcggct tcgagatcag   2820
217 caacgacagc atcaccgtgc tgaaggtgta cgaggccaag ctgaagcaga actaccaggt   2880
219 ggacaaggac agcttgagcg aggtgatcta cggcgacatg gacaagctgc tgtgtccgga   2940
221 ccagagcgag caaatctact acaccaacaa catcgtgttc ccgaacgagt acgtgatcac   3000
223 caagatcgac ttcaccaaga agatgaagac cctgcgctac gaggtgaccg ccaacttcta   3060
225 cgacagcagc accggcgaga tcgacctgaa caagaagaag gtggagagca gcgaggccga   3120
227 gtaccgcacc ctgagcgcga acgacgacgg cgtctacatg ccactgggcg tgatcagcga   3180
229 gaccttcctg accccgatca acggctttgg cctgcaggcc gacgagaaca gccgcctgat   3240
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233 ggagaccaag ctgatcgtgc caccgagcgg cttcatcagc aacatcgtgg agaacggcag   3360
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237 caccggcggc gtgaacggca ccaaggccct gtacgtgcac aaggacggcg gcatcagcca   3480
239 gttcatcggc gacaagctga agccgaagac cgagtacgtg atccagtaca ccgtgaaggg   3540
241 caagccatcg attcacctga aggacgagaa caccggctac atccactacg aggacaccaa   3600
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245 gggcgtgtac ctgatcctga agagccagaa cggcgacgag gcctggggcg acaacttcat   3720
247 catcctggag atcagcccga gcgagaagct gctgagcccg agctgatca acaccaacaa   3780
249 ctggaccagc accggcagca ccaacatcag cggcaacacc ctgaccctgt accagggcgg   3840
251 ccgcggcatc ctgaagcaga acctgcagct ggacagcttc agcacctacc gcgtgtactt   3900
253 cagcgtgagc ggcgacgcca cgtgcgcat ccgcaactcc cgcgaggtgc tgttcgagaa   3960
255 gaggtacatg agcggcgcca aggacgtgag cgagatgttc accaccaagt tcgagaagga   4020
257 caacttctac atcgagctga gccagggcaa caacctgtac ggcggcccga tcgtgcactt   4080
259 ctacgacgtg agcatcaagt aggagctcta gatccccgga atttcccga tcgttcaaac   4140
261 atttggcaat aaagtttctt aagattgaat cctgttgccg gtcttgcgat gattatcata   4200
263 taatttctgt tgaattacgt taagcatgta ataattaaca tgtaatgcat gacgttattt   4260
265 atgagatggg ttttatgat tagagtcccg caattataca tttaatacgc gatagaaaac   4320
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273 <211> LENGTH: 789
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277 <220> FEATURE:
278 <223> OTHER INFORMATION: VIP3A protein motif
280 <400> SEQUENCE: 9
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287             20                  25                  30
290 Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
291         35                  40                  45
294 Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys
295     50                  55                  60
298 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
299 65                  70                  75                  80
302 Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
303                 85                  90                  95
306 Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
307             100                 105                 110
310 Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
311         115                 120                 125
314 Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
315         130                 135                 140
318 Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val
319 145                 150                 155                 160
322 Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
323                 165                 170                 175
326 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
327             180                 185                 190
330 Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu
331         195                 200                 205
334 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
335         210                 215                 220
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338 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
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343             245                 250                 255
346 Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
347         260                 265                 270
350 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe Leu Thr
351         275                 280                 285
354 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
355     290                 295                 300
358 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
359 305                 310                 315                 320
362 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
363             325                 330                 335
366 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
367             340                 345                 350
370 Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr
371         355                 360                 365
374 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
375     370                 375                 380
378 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu
379 385                 390                 395                 400
382 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
383             405                 410                 415
386 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
387         420                 425                 430
390 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
391         435                 440                 445
394 Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
395     450                 455                 460
398 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
399 465                 470                 475                 480
402 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
403             485                 490                 495
406 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
407         500                 505                 510
410 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
411     515                 520                 525
414 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
415     530                 535                 540
418 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
419 545                 550                 555                 560
422 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
423             565                 570                 575
426 Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
427             580                 585                 590
430 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
431         595                 600                 605
434 Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date